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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,298A

DATE: 04/17/2003

TIME: 10:49:15

Input Set : A:\2003-04-07 1254-0191P.ST25.txt
 Output Set: N:\CRF4\04172003\J024298A.raw

3 <110> APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
 4 Akio MATSUDA
 5 Goichi HONDA
 6 Shuji MURAMATSU
 7 Yukiko NAGANO
 9 <120> TITLE OF INVENTION: NF-K B Activating Gene
 11 <130> FILE REFERENCE: 1254-0191P
 13 <140> CURRENT APPLICATION NUMBER: 10/024,298A
 C--> 14 <141> CURRENT FILING DATE: 2003-04-08
 16 <150> PRIOR APPLICATION NUMBER: 60/314,385
 17 <151> PRIOR FILING DATE: 2001-08-24
 19 <150> PRIOR APPLICATION NUMBER: 60/278,641
 20 <151> PRIOR FILING DATE: 2001-03-26
 22 <150> PRIOR APPLICATION NUMBER: 60/258,315
 23 <151> PRIOR FILING DATE: 2000-12-28
 25 <150> PRIOR APPLICATION NUMBER: JP254018/2001
 26 <151> PRIOR FILING DATE: 2001-08-24
 28 <150> PRIOR APPLICATION NUMBER: JP0088912/2001
 29 <151> PRIOR FILING DATE: 2001-03-26
 31 <150> PRIOR APPLICATION NUMBER: JP402288/2000
 32 <151> PRIOR FILING DATE: 2000-12-28
 34 <160> NUMBER OF SEQ ID NOS: 182
 36 <170> SOFTWARE: PatentIn Ver. 2.0
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 48 20 25 30
 50 Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser
 51 35 40 45
 53 Ala Gly Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
 54 50 55 60
 56 Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
 57 65 70 75 80
 59 Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
 60 85 90 95
 62 Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr
 63 100 105 110
 65 Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro

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66 115 120 125
 68 Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser
 69 130 135 140
 71 Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly
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 74 Tyr Gly Gly Thr Arg Arg Arg
 75 165
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 81 <213> ORGANISM: Homo sapiens
 83 <220> FEATURE:
 84 <221> NAME/KEY: CDS
 85 <222> LOCATION: (194)..(694)
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 90 ttcttggtgc ttggagtata atttagatta tacagaactt ggcctgcaga aactgaagga 120
 92 gtctggaaag cagcacggct ttgcctctt ctctgattat tattataagt ggtcctcgcc 180
 94 ggattcctgt aac atg agt gga ttg att acc atc gtg gta ctc ctt ggg 229
 95 Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly
 96 1 5 10
 98 atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct 277
 99 Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser
 100 15 20 25
 102 cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325
 103 Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg
 104 30 35 40
 106 ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc 373
 107 Phe Thr Asn Ser Ala Gly Pro Pro Pro Gly Phe Lys Ser Glu Phe
 108 45 50 55 60
 110 aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt 421
 111 Thr Gly Pro Gln Asn Thr Gly His Ala Thr Ser Gly Phe Gly Ser
 112 65 70 75
 114 gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg 469
 115 Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp
 116 80 85 90
 118 aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat 517
 119 Thr Gly Leu Gly Thr Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn
 120 95 100 105
 122 aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct 565
 123 Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro
 124 110 115 120
 126 ccc tcc tac cct ggc acg tgg aat agg gct tac tca ccc ctt cat gga 613
 127 Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
 128 125 130 135 140
 130 ggc tcg ggc agc tat tcg gta tgt tca aac tca gac acg aaa acc aga 661
 131 Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg
 132 145 150 155
 134 act gca tca gga tat ggt ggt acc agg aga cga taaagttagaa agttggagtc 714

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135 Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
 136 160 165
 138 aaacactgga tgcagaaaatt ttggattttt catcaacttc tcttttagaaa aaaagtacta 774
 140 cctgttaaca attggaaaaa ggggatattc aaaagttcggttggatgttgcgg tccagtgttag 834
 142 cttttgtat tctattattt gaggctaaaa gttatgtgttgcgg gacaaaatac ttatgtgttg 894
 144 tatgtcagttaacatgcag atgtatattt cagttttga aagtgtatcat tactgtggaa 954
 146 tgctaaaaat acattaattt ctaaaacctg tgatgcccta agaagcatta agaatgaagg 1014
 148 tgttgtacta atagaaacta agtacagaaa atttcagttt taggtggttt tagctgtatga 1074
 150 gtttattacact catagagact gtaatatttctt atttggattt atattatgg atgtttgctg 1134
 152 ttcttcaaac atttaaatca agctttggac taattatgtt aatttggat ttctgtatcac 1194
 154 tttttagcttc tgaagctttt aatcatttcag tggggagat ggccttctgg taactgaata 1254
 156 ttacccctcg tagggaaaagg tggaaaataa gcattctagaa ggttggatgtt aatgactctg 1314
 158 tgctggcaaa aatgcttggaa acctctatat ttctttcggtt cataagaggt aaaggtcaaa 1374
 160 tttttcaaca aaagtctttt aataacaaaaa gcatgcagtt ctctgtgaaa tctcaaataat 1434
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 166 <211> LENGTH: 339
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 175 20 25 30
 177 Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
 178 35 40 45
 180 Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
 181 50 55 60
 183 Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
 184 65 70 75 80
 186 Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
 187 85 90 95
 189 Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
 190 100 105 110
 192 Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
 193 115 120 125
 195 Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
 196 130 135 140
 198 Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
 199 145 150 155 160
 201 Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
 202 165 170 175
 204 Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
 205 180 185 190
 207 Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
 208 195 200 205
 210 Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
 211 210 215 220
 213 Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His

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214 225 230 235 240
 216 Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
 217 245 250 255
 219 Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
 220 260 265 270
 222 Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
 223 275 280 285
 225 Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
 226 290 295 300
 228 Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
 229 305 310 315 320
 231 Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
 232 325 330 335
 234 Arg Arg Arg
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 240 <212> TYPE: DNA
 241 <213> ORGANISM: Homo sapiens
 243 <220> FEATURE:
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 245 <222> LOCATION: (115)..(1131)
 247 <400> SEQUENCE: 4
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 250 cccaggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg 117
 251 Met
 252 1
 254 gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
 255 Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Gly
 256 5 10 15
 258 ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc ttg aac gac 213
 259 Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
 260 20 25 30
 262 cct gac aga atg ttg ctg ccg gat gta aaa gct ctt acc ctc cac tat 261
 263 Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
 264 35 40 45
 266 gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
 267 Asp Arg Tyr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
 268 50 55 60 65
 270 tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
 271 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
 272 70 75 80
 274 cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
 275 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
 276 85 90 95
 278 aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
 279 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
 280 100 105 110
 282 tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
 283 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser

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Input Set : A:\2003-04-07 1254-0191P.ST25.txt

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284	115	120	125	
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287	Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys			
288	130	135	140	145
290	ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat			597
291	Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr			
292	150	155	160	
294	tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att			645
295	Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile			
296	165	170	175	
298	acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc			693
299	Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe			
300	180	185	190	
302	ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca			741
303	Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro			
304	195	200	205	
306	ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc			789
307	Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro			
308	210	215	220	225
310	cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt			837
311	Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly			
312	230	235	240	
314	gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa			885
315	Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu			
316	245	250	255	
318	aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta			933
319	Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Ile Leu			
320	260	265	270	
322	gga tat ttg ttt ggc agc aat aga ggc gca aca ccc ttc tca gac tcg			981
323	Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser			
324	275	280	285	
326	tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg			1029
327	Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg			
328	290	295	300	305
330	gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca			1077
331	Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser			
332	310	315	320	
334	aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg			1125
335	Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg			
336	325	330	335	
338	aga cga taaagttagaa agttggagtc aaacactgga tgcagaaatt ttggatttt			1181
339	Arg Arg			
341	catcaacttc tcttttagaaa aaaagtacta cctgttaaca atttggaaaa gggatattc			1241
343	aaaagttcgg tgggttatg tccagtgtat cttttgtat tctattattt gagctaaaa			1301
345	gttcatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattt			1361
347	cagttttga aagtgtatcat tactgtggaa tgctaaaaat acattaattt ctaaaacctg			1421
349	tgtatgcccta agaagcatta agaatgaagg tgggttacta atagaaacta agtacagaaa			1481
351	atttcagtt taggtggttg tagctgtatca gttattacatcatagagact gtaatattct			1541
353	atttggattt atattattttt atgtttgcgtt ttcttcaaac atttaaatca agctttggac			1601

VERIFICATION SUMMARY

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Output Set: N:\CRF4\04172003\J024298A.rawL:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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L:20798 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (180) SEQUENCE: